

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/765,061B

DATE: 02/04/2002

TIME: 13:02:31

Input Set : A:\Copy of SQ-09765061.txt Output Set: N:\CRF3\02042002\1765061B.raw

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2 <110> APPLICANT: Board of Regents of the University of Texas System
4 <120> TITLE OF INVENTION: Mutations in a Novel Photoreceptor-pineal gene 17P cause
        leber congenital amaurosis (LCA4)
7 <130> FILE REFERENCE: 96606/16UTL
8 <140> CURRENT APPLICATION NUMBER: 09/765,061B
9 <141> CURRENT FILING DATE: 2001-01-17
11 <160> NUMBER OF SEQ ID NOS: 78
12 <170> SOFTWARE: PatentIn version 3.1
14 <210> SEQ ID NO: 1
                                                          ENTERED
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16 <212> TYPE: DNA

15 <211> LENGTH: 6689

- 17 <213> ORGANISM: Homo sapiens
- 20 <220> FEATURE:
- 21 <221> NAME/KEY: gene
- 22 <222> LOCATION: (1)..(6689)
- 23 <223> OTHER INFORMATION: the AIPL1 gene produces aryl-hydrocarbon receptor
- 24 interacting protein-like 1
- 26 <220> FEATURE:
- 27 <221> NAME/KEY: misc_feature
- 28 <222> LOCATION: (1897)..(1906)
- 29 <223> OTHER INFORMATION: n represents any of the four nucleotides A T G or C
- 31 <220> FEATURE:
- 32 <221> NAME/KEY: misc_feature
- 33 <222> LOCATION: (3946)..(3946)
- 34 <223> OTHER INFORMATION: n represents any of the four nucleotides A T G or C
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- 39 aagaaagete ageggaeett ttteettett ggggtggaae aaaaageeaa atetageaea 120
- 41 accetgggea ggggeeeaga ateaetggaa geaaaggtgg atqqqataqq aggeqaqqet
- 43 gcctgtggac cacaggcccg gcccgagtgg ctctgatgag aagccggggc gcctaggtca
- 45 cogececcae egtetgeeet tecececaet ecteetgget gggtaaatee cagagtetea
- 47 geogeotaag tgtetteece ggaggtgaga ttateteege etgtgetgga caceteeett
- 49 totoctgoag coatggatgo ogototgoto otgaacgtgg aaggggtoaa gaaaaccatt 420
- 480
- 51 ctgcacgggg gcacgggcga gctcccaaac ttcatcaccg gatcccgagt gagtggggcc
- 53 cctccggagc agacagggtc ccccacagca gctttcaaca ttccaggtgt gccccaaggc 540
- 55 actgtaaaca gettteaget gtgeeaaaaa aacageeagg eageeecage getgggeete 600
- 57 cggggagete ceagegitta eccatteagg gggeattitt ggtaetitge agatteaact 660
- 59 ttagcatggg ctgaggggaa gggcttttgg gaattttctg gggccctaaa tgttgagtga 720
- 61 gaagaaaggg agtccgagga gtcttggtat ttgtccccaa atgtctgtta ggcttccctg
- 63 gactgaaggg tgcgtctgtg gctacagaat tcgggctttg gccaggcgag gcggctcccg
- 65 cctgtaatcc cagcactttg ggaggccaag atgggcagat catgaggtca agagttcgag
- 67 accagectga ccaacatgtg aaaccecate tetactgaaa atacaaaaat tagecagatg
- 69 tgctgtggcg cctgtaatcc cagttcagat actcaggaga cttgaggèag gagaatcact 1020

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71 tgagcccagg aggtggaggt tgcagtgagc cgagatcata ccactgcact ccaacctggg 1080 75 ggaaggattt ctggacgcac agggctgtgg ggagtggaat ggggtctgta gggaggggtg 1200 77 ggtccctcct ccctgggggg tgcaggcagg gtggaggtgc tccaggggtc tgaggcatct 1260 79 gatggggtga actgagtgag ctgaccctgg ggacagccct gggtgtcggt ggcaaggggg 1320 81 tggcttctgc cgggccttga acagtgtgtc tagagcagag tgcaccgtct cggtgactag 1380 83 gtgatettte attteegeae eatgaaatgt gatgaggage ggaeagteat tgaegaeagt 1440 85 cggcaggtgg gccagcccat gcacatcatc atcggaaaca tgttcaagct cgaggtctgg 1500 87 gagateetge ttaecteeat gegggtgeae gaggtggeeg agttetggtg egacaceate 1560 89 gtaagtagge eetgegegee tgteteetgg gactagtett ttetgggete acceaecege 1620 91 tttgcqqqqc tqctqtttt cqqqaaaqct qqqactcaaq cqaaqctttq caaaqccaqt 1680 93 cctgcaaact tattccccac cgtgtgcatg tgaagatgga gggaacaagg gctggaaggg 1740 95 gtgacccatg ctgtggctgg ctggtgggga gcagggctat gaccagcagg agtgagctgg 1800 $^{\prime}$ 97 cecaetteae agtecteaea tetgtgtgtgt tgtgtgtgtg tgtgtgtgtgtgtgtgtg1860 99 tgtgtgtgtg agagagaga agagagagag agagagnnnn nnnnnntagc cttaggactt 1920 101 attgcagaga ccaacaccta acaatgtaat caggcagcca gtgcaggaca taaataagta 1980 103 aggcagtgtg ctttgggcca caaaagcacg ctcagcttgc tggaagccat gggtgccgag 2040 105 ctgggggctg ctgagtcagg gccaaagggg gcccctccct gcagtaaget ggttctgggg 2100 107 cetetecete cettggteca getettaate ceaacagget caacagecat etgettgtet 2160 109 cttccataaa gaggcagaag gcatttcggg ctaatcccgg ccggtggggc gggcagggtg 2220 111 acctctgtct ctgtgctggt gacctggagg cagagctgaa ctgctgcata gagtttcagc 2280 113 cccttcactt cacatgttgc atgtggggcc agtgctgggt catctcagaa gccggtccaa 2340 115 ggagatgggt tctcagggag cctagttggg gaaactgagg cccagcatac atacagcagg 2400 117 cctcgctgag gccgcacggc ggatcttccc agccctcctt catcccaagg gtggcaaact 2460 119 cageteccat getggetgaa getgtgatga gecagateta tatetgeace ateteattta 2520 121 atccctacag cagccctaat atcgaacagg agcaacccag ggaactgagt ttcagagaag 2580 123 tgcagagacc tgggctcacc gctaacctgc agcactgcca ggacaccaaa gcgactctct 2640 125 tggaccetgg agtectgete ettetaetge eccaeaetge cetteetgeg agteatagge 2700 127 tttgcagagg tcagggtttc cctggggcag agatgtgtta cagtggacca caagggccag 2760 129 aagaggcagc cggaggctaa cagcatatgg cctctggagc caggtttgaa tcctggctgc 2820 131 gtcatttcct agctgtgtga ccttaagcaa gttgcttgcg tctctgggct gtagtttccc 2880 133 catccgtaaa atgggataat agtgcctgcc ttgaattgtc ataaggattg aaggggctca 2940 135 taacagtgtg aagtgctttg cctggcacac agttaaccac agttagtatg agtggcatag 3000 137 tgagggagca ggattcctcc caggaggggc tctgagtgga ggccttttat ggcccaccta 3060 139 getetgggea ggtageetgg atgecateea teegtttate eecaeageae aegggggtet 3120 141 accccatect rteeeggage etgaggeaga tggcccaggg caaggaceee acagagtgge 3180 .143 acgtgcacac gtgcgggctg gccaacatgt tcgcctacca cacgctgggc tacgaggacc 3240 145 tggacgaget geagaaggag ceteageete tggtetttgt gategagetg etgeaggtgg 3300 147 ggctggggtt ggcagggctg gagggctgtg ccagcactgg agagggacag cgggcatcat 3360 149 gggcaccccc accccactgg ccactggaca gtgccctgtt tctgtttaga taatacgaga 3420 151 gggttcataa gccatgggag aatacgaatt tgaaaaaaaa gtcctctgat ttttccacaa 3480 153 gaaaagteet ttggtgetgg geatggtgge ceaegeetgt aateetagea etttgggagg 3540 155 ccqaqqqqqt tqqatcacct qaqqtcaqqa qttcqaaqac caqcctqqcc aacatqqtaa 3600 157 aaccccgtct ctattaaaaa cacaaaaatt aaccgggtgt ggtggtgcat gcctgtaatc 3660 159 aatcccagct acttgggaat ttgaggcatg agaattgctt gaacctggaa gtggaggttg 3720 161 cagtgagcag agatcatgtc agtgcatttt aacctgggtg acagagtgag actccatgtc 163 caaaaaaaaq aaaaaaaaaa aaagtccact tggaaccagt ttttaaaaat gtgattcatt 1/65 ttcattgtgg aggcatttta tccacttcca ctttcatttt caggagttgg agattataac 3900 167 cgcctccttg gttcctgtgg tttgtgggtt cagacttggt tctctmgtgg cgggagaggc 3960

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264 <211> LENGTH: 1119 265 <212> TYPE: DNA

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Input Set : A:\Copy of SQ-09765061.txt
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268 <220> FEATURE:
269 <221> NAME/KEY: gene
270 <222> LOCATION: (1)..(1119)
271 <223> OTHER INFORMATION: the AIPL1 gene produces aryl-hydrocarbon receptor
272
          interacting protein-like 1
274 <400> SEQUENCE: 2
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278 acgggcgage teceaaaett cateacegga tecegagtga tettteattt eegeaeeatg
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280 aaatgtgatg aggagegeae ggteategae gaeageegge aggtggaeea geeeatgeae
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282 atcatcatcg ggaacatgtt caagctcgag gtctgggaga tectgetcac ctccatgagg
284 gtgcacgagg tggccgagtt ctggtgcgac accatccaca cgggggtcta ccccatcctg
                                                                         300
286 teceggagee tgeggeagat ggeeeaggge aaggaeeeca eggagtggea egtgeaeaca
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288 tgcgggctgg ccaacatgtt cgcctaccac acactgggct acgaggacct ggacgagctg
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290 cagaaggagc ctcagcctct gatctttgtg atcgagctgc tgcaggttga cgccccgagt
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292 gattaccaga gggagacctg gaacctgagc aatcatgaga agatgaaggt ggtgcccgtc
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294 ctccacggag agggaaatcg gctcttcaag ctgggccgct acgaggaggc ctcttccaag
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296 taccaggagg ccatcatctg cctaaggaac ctgcagacca aggagaagcc atgggaggtg
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298 cagtggctga agctggagaa gatgatcaac accctgaccc tcaactactg ccagtgcctg
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300 ctgaagaagg aggagtatta cgaggtgctg gagcacacca gtgacattct ccggcaccac
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302 ccaggcatcg tgaaggccta ctatgtgcgt gcccgggctc acgcagaggt gtggaatgag
                                                                         840
304 geogaggeea aggeggaeet eeagaaagtg etggagetgg ageeateeat geagaaggeg
                                                                         900
306 gtgcgcaggg agctgaggct gctggagaac cgcatggcag agaagcagga ggaggagcgg
                                                                         960
308 ctgcgctgcc ggaacatgct gagccaggga gccacgcagc ctcccacaga gccaccggca
                                                                        1020
310 gagccccaca cagcaccacc tgcggagctg tccacagggc cacctgcaga gccacccgca
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312 gageteecce tgteeccagg geacteactg cageactga
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317 <211> LENGTH: 1155
318 <212> TYPE: DNA
319 <213> ORGANISM: Pan troglodytes
321 <220> FEATURE: .
322 <221> NAME/KEY: gene
323 <222> LOCATION: (1)..(1155)
324 <223> OTHER INFORMATION: the AIPL1 gene produces aryl-hydrocarbon receptor
325
          interacting protein-like 1
327 <400> SEQUENCE: 3
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330 acgggcgagc tcccaaactt catcaccgga tcccgagtga tctttcattt ccgcaccatg
                                                                         120
332 aaatgtgatg aggagcggac agtcattgac gacagccggc aggtgggcca gcccatgcac
                                                                         180
334 atcatcatcg gaaacatgtt caagctcgag gtctgggaga tcctgcttac ctccatgcgg
                                                                         240
336 qtqcacgagg tggccgagtt ctggtgcgac accatccaca caggggtcta ccccatcctg
                                                                         300
338 teceggagee tgaggeagat ggeecaggge aaggaceeca cagagtggea egtgeacaca
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340 tgcgggctgg ccaacatgtt cgcctaccac acqctqqqct acgaggacct ggacqaqctq
                                                                         420
342 cagaaggage cteageetet ggtetttgtg ateqagetge tgeaggttga tgeeeggagt
                                                                         480
344 gattaccaga gggagacctg gaacctgagc aatcatgaga agatgaaggc ggtgcccqtc
                                                                         540
346 ctccacggrg agggaaatcg gctcttcaag ctgggacgct acgaggaggc ctcttccaag
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348 taccaggagg ccatcatctg cctaaggaac ctgcagacca aggagaagcc gtgggaggtg
                                                                         660
350 cagtggctga agctggagaa gatgatcaat actctgatcc tcaactactg ccagtgcctg
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352 ctgaagaagg aggagtacta tgaggtgctg gagcacacca gcgacattct ccggcaccac
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354 ccaggeateg tgaaggeeta etaegtgegt geeegggete aegeagaggt gtggaatgag
                                                                         840
356 gccgaggcca aggcagacct ccggaaagtg ctggagctgg agccgtccat gcagaaggcg
                                                                         900
358 gtgcgcaggg agctgaggct gctggagaac cgcatggcgg agaagcagga ggaggagcgg
                                                                         960
360 ctgcgctgcc ggaacatgct gagccagggt gccacgcagc ctccggcaga gccacccaca
                                                                        1020
362 gagecacceg cacagteate cacagageca ectgeagage cacececage accatetgea
                                                                        1080
364 gagetgteeg cagggeeace tgeagagaea geeacagage caececegte eecagggeac
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366 tegetgeage actga
                                                                        1155 -
370 <210> SEQ ID NO: 4
371 <211> LENGTH: 1060
372 <212> TYPE: DNA
373 <213> ORGANISM: Bos taurus
375 <220> FEATURE:
376 <221> NAME/KEY: gene
377 <222> LOCATION: (1)..(1060)
378 <223> OTHER INFORMATION: the AIPL1 gene produces aryl-hydrocarbon receptor
          interacting protein-like 1
381 <400> SEQUENCE: 4
382 atggatgeca etetgeteet gaatgtggaa gggateaaga aaaccattet geatggggge
                                                                          60
384 acaggggacc tececaactt cattactgga geeegagtga cettteattt eegaaceatg
                                                                         120
386 aaatgtgatg aggagcggac ggtgatagac gacagcaagc aggtgggcca tcccatgcac
                                                                         180
388 atcatcattg ggaacatgtt caagctggag gtctgggaga tcttgctgac gtccatgcgg
                                                                         240
390 gtcagcgagg tggccgagtt ttggtgcgac accatccaca caggggtcta ccccatcctg
                                                                         300
392 teceggagee tgeggeagat ggeggagggt aaggaceeca cagagtggea egtgeacaeg
                                                                         360
394 tgtggcttgg ccaacatgtt cgcttaccac acqctgggct acqaggacct ggacqagctg
                                                                         420
396 cagaaggage cteageeact gatetteata ategagttge tgeaggtega ggeeeegage
                                                                         480
398 cagtaccaga gggagacctg gaacctgaat aaccaggaga agatgcaggc ggtgcccatc
                                                                         540
                                                                         600
400 ctccatggag aaggaaaccg gctcttcaag ctgggccgct acgaggaggc ctccaacaag
402 taccaggaag ccatcgtctg cctgaggaac ctgcagacca aggagaaacc ctgggaggtg
                                                                         660
404 cagtggctga agctggagaa gatgatcaac accctgatcc tgaactactg tcagtgtctg
                                                                         720
406 ctgaagaagg aggagtacta cgaggtgctg gaacacacta gtgacatcct ccggcatcac
                                                                         780
408 ccaggcatcg tgaaggccta ctatgtgagg gcccgggctc acgccgaggt gtggaatgag
                                                                         840
410 geggaageea aggeggatet ggagaaagtg etggagetgg ageegteeat geggaaggeg
                                                                         900
412 qtqcaqaqqq aqctqaqqct qctqqaqaac cqqctqqaqq aqaaacqcqa qqaqqaqcqa
                                                                         960
414 ctgcgctgcc ggaacatgct gggctagtgc gcaggcgcca agcctcctgc ctccgcccc
                                                                        1020
416 cgcycctcca cccccccaa aaaaaaaaaa aaaaattttt
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419 <210> SEQ ID NO: 5
420 <211> LENGTH: 925
421 <212> TYPE: DNA
422 <213> ORGANISM: Canis familiaris
424 <220> FEATURE:
425 <221> NAME/KEY: gene
426 <222> LOCATION: (1)..(925)
427 <223> OTHER INFORMATION: the AIPL1 gene produces ary1-hydrocarbon receptor
428
          interacting protein-like 1
430 <400> SEQUENCE: 5
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                                                                          60
433 teegeacaae gaaatgegae gaggegegga eagtgatega egacageaag egtgtgggee
                                                                         120
435 atcccatgca catcatcatc gggaacatgt tcaagctgga ggtctgggag gtgctgctga
                                                                         180
437 catecatgeg egtgggegag gtggeegagt tetggtgega etetatteae acaggagtet
                                                                         240
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Use of n and/or Xaa has been detected in the Sequence Listing.

Review the Sequence Listing to insure a corresponding explanation is presented in the <220> to <223> fields of each sequence using n or Xaa.

VERIFICATION SUMMARY

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Input Set : A:\Copy of SQ-09765061.txt
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L:8 M:283 W: Missing Blank Line separator, <140> field identifier

L:99 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 L:167 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 L:1717 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:72